WHAT IS CLAIMED IS:

1. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 1: 1-70715, 70795-82207, 82297-83612, 83824-85297, 85418-86388, 86446-87495, 87523-88294, 88384-89483, 89650-92748, 97156-98309, 98476-99329, 99491-100026, 100212-100281, 100396-100538, 100682-100833, 100995-101920, 102087-102970, 103264-103724, and 103753-106746.

2. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide G at positions 70728, 87860, 88297, 94432, and 95340 of SEQ ID No. 1; a nucleotide A at positions 82218, 83644, 83808, 87787, 87806, 94218, and 97144 of SEQ ID No. 1; a nucleotide C at positions 87902, 88215, 88283, 92760, 93726, and 94422 of SEQ ID No. 1; and a nucleotide T at positions 93903, and 94170 of SEQ ID No. 1.

3. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises a nucleotide G at positions 86435, 93592, 93680, 93681, 93682, 93728, 93761, and 95445 of SEQ ID No. 1; a nucleotide A at positions 86434, 88355, 93240, 93471, and 93747of SEQ ID No. 1; a nucleotide C at positions 93683, 95126, and 95444 of SEQ ID No. 1; and a nucleotide T at positions 94154, and 94430 of SEQ ID No. 1.

4. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 1: 92975-92977, 93711-93715, 94151-94153, 94240-94243, 94770-94773, 94804-94808, 95121-95122, 95129-95135, 95148-95153, 95154-95159, 95173-95178, 95367-95374, 95410-95413, 95418-95420, 95430-95436, 95533-95535, and 95677-95677.

5. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least 1 of the nucleotide positions 1-162 of SEQ ID No. 2.

6. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2471, and 5397 of SEQ ID No. 2; a nucleotide C at

positions 1013, 1979, and 2675 of SEQ ID No. 2; a nucleotide G at positions 176, 749, 2685, 3593 of SEQ ID No. 2; and a nucleotide T at positions 2156, and 2423 of SEQ ID No. 2.

7. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708, 807, 1493, 1724, and 2000; a nucleotide C at positions 1936, 3379, and 3697; a nucleotide G at positions 709, 1845, 1933, 1934, 1935, 1981, 2014, and 3698; and a nucleotide T at positions 2407, and 2683 of SEQ ID No. 2.

8. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 2: 1229-1231, 1964-1968, 2404-2406, 2493-2496, 3023-3026, 3057-3061, 3374-3375, 3382-3388, 3401-3406, 3407-3412, 3426-3431, 3620-3627, 3663-3666, 3671-3673, 3683-3689, 3786-3788, and 3930-3932.

9. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 3: 1-162 and 747-872.

10. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2597, and 3523 of SEQ ID No. 3; a nucleotide C at positions 1139, 2105, and 2801 of SEQ ID No. 3; a nucleotide G at positions 176, 875, 2811, 3719 of SEQ ID No. 3; and a nucleotide T at positions 2282, and 2549 of SEQ ID No. 3.

11. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708, 807, 1619, 1850, and 2126; a nucleotide C at positions 2062, 3505, and 3823; a nucleotide G at positions 709, 1971, 2059, 2060, 2061, 2107, 2140, and 3824; and a nucleotide T at positions 2533, and 2809 of SEQ ID No. 3.

12. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 3: 1355-1357, 1892-1894, 2090-2094, 2530-2532, 2619-

2622, 3149-3152, 3183-3187, 3500-3501, 3508-3514, 3527-3532, 3533-3538, 3552-3557, 3746-3749, 3789-3792, 3797-3799, 3809-3815, 3912-3914 and 4056-4058.

13. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least 1 of the nucleotide positions 1-162 of SEQ ID No. 4.

14. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527 and 2460 of SEQ ID No. 4; a nucleotide C at position 1013 of SEQ ID No. 4 and a nucleotide G at positions 176, and 749 of SEQ ID No. 4.

15. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708 and 807 and a nucleotide G at position 709 of SEQ ID No. 4.

16. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises the pairs of nucleotide positions 1136-1137 of SEQ ID No. 4.

17. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID No.s 1, 2, 3, and 4 or the complement thereof, wherein said span includes a *PCTA-1*-related biallelic marker in said sequence.

18. A polynucleotide according to claim 17, wherein said *PCTA-1*-related biallelic marker is selected from the group consisting of A1 to A125, and the complements thereof.

19. A polynucleotide according to claim 17, wherein said *PCTA-1*-related biallelic marker is selected from the group consisting of A1 to A44, A46 to A53, A57, A58, A62 to A76, A81, A82, A86 to A91, A107, A118, and A123 to A125, and the complements thereof.

20. A polynucleotide according to claim 14, wherein said *PCTA-1*-related biallelic marker is selected from the group consisting of A45, A54, A60, A61, A77 to A80, A83 to A85, A93, A102 to A106, A109, A110, A114, and A122, and the complements thereof.

21. A polynucleotide according to claim 17, wherein said *PCTA-1*-related biallelic marker is selected from the group consisting of A55, A56, A59, A92, A94 to A101, A108, A111 to A113, A115 to A117, and A119 to A121, and the complements thereof.

22. A polynucleotide according to any one of claims 17 to 21, wherein said contiguous span is 18 to 47 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.

23. A polynucleotide according to claim 22, wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

24. A polynucleotide according to claim 22, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: P1 to P125, and the complementary sequences thereto.

25. A polynucleotide according to any one of claims 1 to 21, wherein the 3' end of said contiguous span is present at the 3' end of said polynucleotide.

26. A polynucleotide according to any one of claims 17 to 21, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide and said biallelic marker is present at the 3' end of said polynucleotide.

27. A polynucleotide according to any one of claims 17 to 21, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a *PCTA-1*-related biallelic marker in said sequence.

28. A polynucleotide according to claim 27, wherein the 3' end of said polynucleotide is located 1 nucleotide upstream of said *PCTA-1*-related biallelic marker in said sequence.

29. A polynucleotide according to claim 28, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: D1 to D125, and E1 to E125.

30. An isolated, purified, or recombinant polynucleotide consisting essentially of a sequence selected from the following sequences: B1 to B47 and C1 to C47.

31. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 5, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 5; and/or
- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 5.

32. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 6, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 245 in SEQ ID No. 6; and/or

- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 225 in SEQ ID No. 6; and/or

- at least 1 of the amiNo. acid encoded by the exon 6bis, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 183-224 of the SEQ ID No. 6.

33. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 7, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 7; and/or

- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 7; and/or

- at least 1 of the amiNo. acid encoded by the exons 9bis and 9ter, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 313-368 of the SEQ ID No. 7.

34. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 8 or the complements thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 8: 1-500, 501-1000, 1001-1500, and 1501-1738.

35. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 9, wherein said contiguous span comprises at least 1 of the following amiNo. acid positions of SEQ ID No. 9: 1-50, 51-100, 101-150, 151-200, 201-250, and 251-316.

36. A polynucleotide for use in a hybridization assay for determining the identity of the nucleotide at a *PCTA-1*-related biallelic marker or the complement thereof.

37. A polynucleotide for use in a sequencing assay for determining the identity of the nucleotide at a *PCTA-1*-related biallelic marker or the complement thereof.

38. A polynucleotide for use in an enzyme-based mismatch detection assay for determining the identity of the nucleotide at a *PCTA-1*-related biallelic marker or the complement thereof.

39. A polynucleotide for use in amplifying a segment of nucleotides comprising a *PCTA-1*-related biallelic marker or the complement thereof.

40. A polynucleotide according to any one of claims 1 to 39 attached to a solid support.

41. An array of polynucleotides comprising at least one polynucleotide according to claim 37.

42. An array according to claim 41, wherein said array is addressable.

43. A polynucleotide according to any one of claims 1 to 39 further comprising a label.

44. A recombinant vector comprising a polynucleotide according to any one of claims 1 to 16, and 31 to 35.

45. A host cell comprising a recombinant vector according to claim 44.

46. A No.n-human host animal or mammal comprising a recombinant vector according to claim 44.

47. A mammalian host cell comprising a *PCTA-1* gene disrupted by homologous recombination with a kNo.ck out vector, comprising a polynucleotide according to any one of claims 1 to 16, and 31 to 35.

48. A No.n-human host mammal comprising a *PCTA-1* gene disrupted by homologous recombination with a kNo.ck out vector, comprising a polynucleotide according to any one of claims 1 to 16, and 31 to 35.

49. A method of geNo.typing comprising determining the identity of a nucleotide at a *PCTA-1*-related biallelic marker or the complement thereof in a biological sample.

50. A method according to claim 49, wherein said biological sample is derived from a single subject.

51. A method according to claim 50, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said individual's geNo.me.

52. A method according to claim 49, wherein said biological sample is derived from multiple subjects.

53. A method according to claim 49, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.

54. A method according to claim 53, wherein said amplifying is performed by PCR.

55. A method according to claim 49, wherein said determining is performed by a hybridization assay.

56. A method according to claim 49, wherein said determining is performed by a sequencing assay.

57. A method according to claim 49, wherein said determining is performed by a microsequencing assay.

58. A method according to claim 49, wherein said determining is performed by an enzyme-based mismatch detection assay.

59. A method of estimating the frequency of an allele of a *PCTA-1*-related biallelic marker in a population comprising:

a) geNo.typing individuals from said population for said biallelic marker according to the method of claim 49; and

b) determining the proportional representation of said biallelic marker in said population..

60. A method of detecting an association between a geNo.type and a trait, comprising the steps of:

a) determining the frequency of at least one *PCTA-1*-related biallelic marker in trait positive population according to the method of claim 59;

b) determining the frequency of at least one *PCTA-1*-related biallelic marker in a control population according to the method of claim 59; and

c) determining whether a statistically significant association exists between said geNo.type and said trait.

61. A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:

a) geNo.typing at least one *PCTA-1*-related biallelic marker according to claim 50 for each individual in said population;

b) geNo.typing a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the geNo.me of each individual in said population; and

c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

62. A method according to claim 61, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark algorithm, or an expectation-maximization algorithm.

63. A method of detecting an association between a haplotype and a trait, comprising the steps of:

a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 62;

b) estimating the frequency of said haplotype in a control population according to the method of claim 62; and

c) determining whether a statistically significant association exists between said haplotype and said trait.

64. A method according to claim 60, wherein said geNo.typing steps a) and b) are performed on a single pooled biological sample derived from each of said populations.

65. A method according to claim 60, wherein said geNo.typing steps a) and b) performed separately on biological samples derived from each individual in said populations.

66. A method according to either claim 60 or 63, wherein said trait is cancer, prostate cancer, an early onset of prostate cancer, a beneficial response to or side effects related to treatment or a vaccination against prostate cancer, a susceptibility to prostate cancer, the level of aggressiveness of prostate cancer tumors, a modified or forthcoming expression of the *PCTA-1* gene, a modified or forthcoming production of the PCTA-1 protein, or the production of a modified PCTA-1 protein.

67. A method according to claim 66 wherein said trait is prostate cancer.

68. A method according to either claim 60 or 63, wherein said control population is a trait negative population.

69. A method according to either claim 60 or 63, wherein said case control population is a random population.

70. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 5, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 5; and/or
- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 5.

71. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 6, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 245 in SEQ ID No. 6; and/or
- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at

amiNo. acid position 55 and an arginine residue at amiNo. acid position 225 in SEQ ID No. 6; and/or

- at least 1 of the amiNo. acid encoded by the exon 6bis, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 183-224 of the SEQ ID No. 6.

72. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 7, wherein said contiguous span includes:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 7; and/or

- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 7; and/or

- at least 1 of the amiNo. acid encoded by the exons 9bis and 9ter, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 313-368 of the SEQ ID No. 7.

73. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amiNo. acids of SEQ ID No. 9, wherein said contiguous span comprises at least 1 of the following amiNo. acid positions of SEQ ID No. 9: 1-50, 51-100, 101-150, 151-200, 201-250, and 251-316.

74. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 70, wherein said epitope comprises:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 5; and/or

- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 5.

75. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 71, wherein said epitope comprises:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 245 in SEQ ID No. 6; and/or

- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at

amiNo. acid position 55 and an arginine residue at amiNo. acid position 225 in SEQ ID No. 6; and/or

- at least 1 of the amiNo. acid encoded by the exon 6bis, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 183-224 of the SEQ ID No. 6.

76. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 72, wherein said epitope comprises:

- a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 7; and/or
- at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 7; and/or
- at least 1 of the amiNo. acid encoded by the exons 9bis and 9ter, more particularly at least 1, 2, 3, 5 or 10 of the amiNo. acid positions 313-368 of the SEQ ID No. 7.

77. An isolated or purified antibody composition are capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 73, wherein said epitope comprises at least 1 of the following amiNo. acid positions of SEQ ID No. 9: 1-50, 51-100, 101-150, 151-200, 201-250, and 251-316.

78. A method of determining whether an individual is at risk of developing prostate cancer, comprising:

a) geNo.typing at least one *PCTA-1*-related biallelic marker according to the method of claim 51; and

b) correlating the result of step a) with a risk of developing prostate cancer.

79. A method according to any one of claims 49, 59, 60, 61, 63, and 78 wherein said *PCTA-1*-related biallelic marker is selected from the group consisting of A1 to A125 and the complements thereof.

80. A method according to claim 78, wherein said *PCTA-1*-related biallelic marker is selected from the following list of biallelic markers: A2, A30, A41, A55 and A57, and the complements thereof.

81. A diagNo.stic kit comprising a polynucleotide according to any one of claims 17 to 30, 40 and 43.

82. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 1: 1-70715, 70795-82207, 82297-83612, 83824-85297, 85418-86388, 86446-87495, 87523-88294, 88384-89483, 89650-92748, 97156-98309, 98476-99329, 99491-100026, 100212-100281, 100396-100538, 100682-100833, 100995-101920, 102087-102970, 103264-103724, and 103753-106746;

b) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide G at positions 70728, 87860, 88297, 94432, and 95340 of SEQ ID No. 1; a nucleotide A at positions 82218, 83644, 83808, 87787, 87806, 94218, and 97144 of SEQ ID No. 1; a nucleotide C at positions 87902, 88215, 88283, 92760, 93726, and 94422 of SEQ ID No. 1; and a nucleotide T at positions 93903, and 94170 of SEQ ID No. 1;

c) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide G at positions 86435, 93592, 93680, 93681, 93682, 93728, 93761, and 95445 of SEQ ID No. 1; a nucleotide A at positions 86434, 88355, 93240, 93471, and 93747of SEQ ID No. 1; a nucleotide C at positions 93683, 95126, and 95444 of SEQ ID No. 1; and a nucleotide T at positions 94154, and 94430 of SEQ ID No. 1;

d) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 1: 92975-92977, 93711-93715, 94151-94153, 94240-94243, 94770-94773, 94804-94808, 95121-95122, 95129-95135, 95148-95153, 95154-95159, 95173-95178, 95367-95374, 95410-95413, 95418-95420, 95430-95436, 95533-95535, and 95677-95677;

e) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the nucleotide positions 1-162 of SEQ ID No. 2;

f) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2471, and 5397 of SEQ ID No. 2; a nucleotide C at positions 1013, 1979, and 2675 of SEQ ID No. 2; a nucleotide G at positions 176, 749, 2685, 3593 of SEQ ID No. 2; and a nucleotide T at positions 2156, and 2423 of SEQ ID No. 2;

g) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708, 807, 1493, 1724, and 2000; a nucleotide C at positions 1936, 3379, and 3697; a nucleotide G at positions 709, 1845, 1933, 1934, 1935, 1981, 2014, and 3698; and a nucleotide T at positions 2407, and 2683 of SEQ ID No. 2;

h) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 2: 1229-1231, 1964-1968, 2404-2406, 2493-2496, 3023-3026, 3057-3061, 3374-3375, 3382-3388, 3401-3406, 3407-3412, 3426-3431, 3620-3627, 3663-3666, 3671-3673, 3683-3689, 3786-3788 and 3930-3932;

i) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 3: 1-162 and 747-872;

j) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2597, and 5523 of SEQ ID No. 3; a nucleotide C at positions 1139, 2105, and 2801 of SEQ ID No. 3; a nucleotide G at positions 176, 875, 2811, 3719 of SEQ ID No. 3; and a nucleotide T at positions 2282, and 2549 of SEQ ID No. 3;

k) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group

consisting of a nucleotide A at positions 708, 807, 1619, 1850, and 2126; a nucleotide C at positions 2062, 3505, and 3823; a nucleotide G at positions 709, 1971, 2059, 2060, 2061, 2107, 2140, and 3824; and a nucleotide T at positions 2533, and 2809 of SEQ ID No. 3;

l) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 3: 1355-1357, 1892-1894, 2090-2094, 2530-2532, 2619-2622, 3149-3152, 3183-3187, 3500-3501, 3508-3514, 3527-3532, 3533-3538, 3552-3557, 3746-3749, 3789-3792, 3797-3799, 3809-3815, 3912-3914 and 4056-4058;

m) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the nucleotide positions 1-162 of SEQ ID No. 4;

n) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527 and 2460 of SEQ ID No. 4; a nucleotide C at position 1013 of SEQ ID No. 4 and a nucleotide G at positions 176, and 749 of SEQ ID No. 4;

o) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708 and 807 and a nucleotide G at position 709 of SEQ ID No. 4;

p) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises the pairs of nucleotide positions 1136-1137 of SEQ ID No. 4;

q) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 8 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 8: 1-500, 501-1000, 1001-1500, and 1501-1738; and,

r) a nucleotide sequence complementary to any one of the preceding nucleotide sequences.

83. A computer readable medium having stored thereon a sequence consisting of a polypeptide code comprising:

a) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 5, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 5; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 5;

b) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 6, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 245 in SEQ ID No. 6; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 225 in SEQ ID No. 6; and/or

iii) at least 1 of the amiNo. acid positions 183-224 of the SEQ ID No. 6;

c) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 7, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 7; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 7; and/or

iii) at least 1 of the amiNo. acid positions 313-368 of the SEQ ID No. 7; and,

d) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 9.

84. A computer system comprising a processor and a data storage device wherein said data storage device a computer readable medium according to with claim 82 or 83.

85. A computer system according to claim 84, further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

86. A computer system of Claim 85 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

87. A computer system of Claim 84 further comprising an identifier which identifies features in said sequence.

88. A method for comparing a first sequence to a reference sequence, comprising the steps of:

reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 1: 1-70715, 70795-82207, 82297-83612, 83824-85297, 85418-86388, 86446-87495, 87523-88294, 88384-89483, 89650-92748, 97156-98309, 98476-99329, 99491-100026, 100212-100281, 100396-100538, 100682-100833, 100995-101920, 102087-102970, 103264-103724, and 103753-106746;

b) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide G at positions 70728, 87860, 88297, 94432, and 95340 of SEQ ID No. 1; a nucleotide A at positions 82218, 83644, 83808, 87787, 87806, 94218, and 97144 of SEQ ID No. 1; a nucleotide C at positions 87902, 88215, 88283, 92760, 93726, and 94422 of SEQ ID No. 1; and a nucleotide T at positions 93903, and 94170 of SEQ ID No. 1;

c) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide G at positions 86435, 93592, 93680, 93681, 93682, 93728, 93761, and 95445 of SEQ ID No. 1; a nucleotide A at positions 86434, 88355, 93240, 93471, and 93747of SEQ ID No. 1; a

nucleotide C at positions 93683, 95126, and 95444 of SEQ ID No. 1; and a nucleotide T at positions 94154, and 94430 of SEQ ID No. 1;

d) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 1 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 1: 92975-92977, 93711-93715, 94151-94153, 94240-94243, 94770-94773, 94804-94808, 95121-95122, 95129-95135, 95148-95153, 95154-95159, 95173-95178, 95367-95374, 95410-95413, 95418-95420, 95430-95436, 95533-95535, and 95677-95677;

e) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the nucleotide positions 1-162 of SEQ ID No. 2;

f) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2471, and 5397 of SEQ ID No. 2; a nucleotide C at positions 1013, 1979, and 2675 of SEQ ID No. 2; a nucleotide G at positions 176, 749, 2685, 3593 of SEQ ID No. 2; and a nucleotide T at positions 2156, and 2423 of SEQ ID No. 2;

g) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708, 807, 1493, 1724, and 2000; a nucleotide C at positions 1936, 3379, and 3697; a nucleotide G at positions 709, 1845, 1933, 1934, 1935, 1981, 2014, and 3698; and a nucleotide T at positions 2407, and 2683 of SEQ ID No. 2;

h) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 2 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 2: 1229-1231, 1964-1968, 2404-2406, 2493-2496, 3023-3026, 3057-3061, 3374-3375, 3382-3388, 3401-3406, 3407-3412, 3426-3431, 3620-3627, 3663-3666, 3671-3673, 3683-3689, 3786-3788 and 3930-3932;

i) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 3: 1-162 and 747-872;

j) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527, 2597, and 5523 of SEQ ID No. 3; a nucleotide C at positions 1139, 2105, and 2801 of SEQ ID No. 3; a nucleotide G at positions 176, 875, 2811, 3719 of SEQ ID No. 3; and a nucleotide T at positions 2282, and 2549 of SEQ ID No. 3;

k) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708, 807, 1619, 1850, and 2126; a nucleotide C at positions 2062, 3505, and 3823; a nucleotide G at positions 709, 1971, 2059, 2060, 2061, 2107, 2140, and 3824; and a nucleotide T at positions 2533, and 2809 of SEQ ID No. 3;

l) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 3 or the complements thereof, wherein said contiguous span comprises nucleotide positions selected from the group consisting of the nucleotide positions of SEQ ID No. 3: 1355-1357, 1892-1894, 2090-2094, 2530-2532, 2619-2622, 3149-3152, 3183-3187, 3500-3501, 3508-3514, 3527-3532, 3533-3538, 3552-3557, 3746-3749, 3789-3792, 3797-3799, 3809-3815, 3912-3914 and 4056-4058;

m) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the nucleotide positions 1-162 of SEQ ID No. 4;

n) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 253, 363, 527 and 2460 of SEQ ID No. 4; a nucleotide C at position 1013 of SEQ ID No. 4 and a nucleotide G at positions 176, and 749 of SEQ ID No. 4;

o) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises at least one nucleotide selected from the group consisting of a nucleotide A at positions 708 and 807 and a nucleotide G at position 709 of SEQ ID No. 4;

p) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 4 or the complements thereof, wherein said contiguous span comprises the pairs of nucleotide positions 1136-1137 of SEQ ID No. 4;

q) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 8 or the complements thereof, wherein said contiguous span comprises at least 1, 2, 3, 5, or 10 of the following nucleotide positions of SEQ ID No. 8: 1-500, 501-1000, 1001-1500, and 1501-1738; and,

r) a nucleotide sequence complementary to any one of the preceding nucleotide sequences; and,

a polypeptide code comprising:

a) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 5, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 5; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 5;

b) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 6, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 245 in SEQ ID No. 6; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 225 in SEQ ID No. 6; and/or

iii) at least 1 of the amiNo. acid positions 183-224 of the SEQ ID No. 6;

c) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 7, wherein said contiguous span includes:

i) a serine residue at amiNo. acid position 170 and/or a lysine residue at amiNo. acid position 203 in SEQ ID No. 7; and/or

ii) at least one residue selected from the group consisting of a tyrosine residue at amiNo. acid position 18, a cysteine residue at amiNo. acid position 35, a methionine residue at amiNo. acid position 55 and an arginine residue at amiNo. acid position 183 in SEQ ID No. 7; and/or

iii) at least 1 of the amiNo. acid positions 313-368 of the SEQ ID No. 7; and,

d) a contiguous span of at least 6 amiNo. acids of SEQ ID No. 9.

ADD A1

add B5

add C2